**What is claimed is:**

1. Process for the preparation of L-amino acids, in particular L-threonine, wherein the following steps are carried out:

   a) fermentation of microorganisms of the Enterobacteriaceae family which produce the desired L-amino acid and in which the yjgF ORF or the nucleotide sequence which codes for it are attenuated, in particular eliminated, and

   b) concentration of the desired L-amino acid in the medium or in the cells of the microorganisms.

2. Process according to claim 1, wherein the desired L-amino acid is isolated, constituents of the fermentation broth and/or the biomass in its entirety or portions (> 0 to 100 %) thereof optionally remaining in the product.

3. Process for the preparation of L-amino acids, in particular L-threonine, or feedstuffs additives comprising these compounds by fermentation of microorganisms of the Enterobacteriaceae family, wherein the yjgF ORF or nucleotide sequences which code for this are attenuated, in particular eliminated, in these and the desired product is isolated.

4. Process according to claim 1, 2 or 3, wherein the activity or concentration of the yjgF ORF gene product is reduced to 0 to 75% of the activity or concentration of the wild-type protein or in the starting microorganism by the attenuation of the yjgF ORF.

5. Process according to claim 1, 2 or 3, wherein microorganisms in which further genes of the biosynthesis pathway of the desired L-amino acid are additionally enhanced are employed.

6. Process according to claim 1, 2 or 3, wherein microorganisms in which the metabolic pathways which reduce the formation of the desired L-amino acid are at least partly eliminated are employed.

7. Process according to claim 1, 2 or 3, wherein the expression of the polynucleotide which codes for the product of the open reading frame yjgF is attenuated, in particular eliminated.

8. Process according to claim 1 or 4, wherein the regulatory and/or catalytic properties of the polypeptide (enzyme protein) for which the polynucleotide of the open reading frame yjgF codes are reduced.

9. Process for the preparation of L-amino acids according to claim 1 or 3, wherein microorganisms of the Enterobacteriaceae family in which additionally at the same time one or more of the genes chosen from the group consisting of:

9.1 the thrABC operon which codes for aspartate kinase, homoserine dehydrogenase, homoserine kinase and threonine synthase,

9.2 the pyc gene which codes for pyruvate carboxylase,

9.3 the pps gene which codes for phosphoenol pyruvate synthase,

9.4 the ppc gene which codes for phosphoenol pyruvate carboxylase,

9.5 the pntA and pntB genes which code for transhydrogenase,

9.6 the rhtB gene which imparts homoserine resistance,

9.7 the mqo gene which codes for malate:quinone oxidoreductase,

9.8 the rhtC gene which imparts threonine resistance,

9.9 the thrE gene which codes for the threonine export protein,

9.10 the gdhA gene which codes for glutamate dehydrogenase,

9.11 the hns gene which codes for the DNA-binding protein HLP-II,

9.12 the pgm gene which codes for phosphoglucomutase,

9.13 the fba gene which codes for fructose biphosphate aldolase,

9.14 the ptsH gene which codes for the phosphohistidine protein hexose phosphotransferase,

9.15 the ptsI gene which codes for enzyme I of the phosphotransferase system,

9.16 the crr gene which codes for the glucose-specific IIA component,

9.17 the ptsG gene which codes for the glucose-specific IIBC component,

9.18 the lrp gene which codes for the regulator of the leucine regulon,

9.19 the csrA gene which codes for the global regulator Csr,

9.20 the fadR which codes for the regulator of the fad regulon,

9.21 the iclR gene which codes for the regulator of central intermediate metabolism,

9.22 the mopB gene which codes for 10 Kd chaperone,

9.23 the ahpC gene which codes for the small sub-unit of alkyl hydroperoxide reductase,

9.24 the ahpF gene which codes for the large sub-unit of alkyl hydroperoxide reductase,

9.25 the cysK gene which codes for cysteine synthase A,

9.26 the cysB gene which codes for the regulator of the cys regulon,

9.27 the cysJ gene which codes for the flavoprotein of NADPH sulfite reductase,

9.28 the cysI gene which codes for the haemoprotein of NADPH sulfite reductase,

9.29 the cysH gene which codes for adenylyl sulfate reductase,

9.30 the phoB gene which codes for the positive regulator PhoB of the pho regulon,

9.31 the phoR gene which codes for the sensor protein of the pho regulon,

9.32 the phoE gene which codes for protein E of the outer cell membrane,

9.33 the pykF gene which codes for fructose-stimulated pyruvate kinase I,

9.34 the pfkB gene which codes for 6-phosphofructokinase II,

9.35 the malE gene which codes for the periplasmic binding protein of maltose transport,

9.36 the sodA gene which codes for superoxide dismutase,

9.37 the rseA gene which codes for a membrane protein with anti-sigmaE activity,

9.38 the rseC gene which codes for a global regulator of the sigmaE factor,

9.39 the sucA gene which codes for the decarboxylase sub-unit of 2-ketoglutarate dehydrogenase,

9.40 the sucB gene which codes for the dihydrolipoyltranssuccinase E2 sub-unit of 2-ketoglutarate dehydrogenase,

9.41 the sucC gene which codes for the β-sub-unit of succinyl-CoA synthetase,

9.42 the sucD gene which codes for the α-sub-unit of succinyl-CoA synthetase,

9.43 the adk gene which codes for adenylate kinase,

9.44 the hdeA gene which codes for a periplasmic protein with a chaperonin-like function,

9.45 the hdeB gene which codes for a periplasmic protein with a chaperonin-like function,

9.46 the icd gene which codes for isocitrate dehydrogenase,

9.47 the mglB gene which codes for the periplasmic, galactose-binding transport protein,

9.48 the lpd gene which codes for dihydrolipoamide dehydrogenase,

9.49 the aceE gene which codes for the E1 component of the pyruvate dehydrogenase complex,

9.50 the aceF gene which codes for the E2 component of the pyruvate dehydrogenase complex,

9.51 the pepB gene which codes for aminopeptidase B,

9.52 the aldH gene which codes for aldehyde dehydrogenase,

9.53 the bfr gene which codes for the iron storage homoprotein,

9.54 the udp gene which codes for uridine phosphorylase, and

9.55 the rseB gene which codes for the regulator of sigmaE factor activity

is or are enhanced, in particular over-expressed, are fermented.

10. Process for the preparation of L-amino acids according to claim 1 or 3, wherein microorganisms of the Enterobacteriaceae family in which additionally at the same time one or more of the genes chosen from the group consisting of:

10.1 the tdh gene which codes for threonine dehydrogenase,

10.2 the mdh gene which codes for malate dehydrogenase,

10.3 the gene product of the open reading frame (orf) yjfA,

10.4 the gene product of the open reading frame (orf) ytfP,

10.5 the pckA gene which codes for phosphoenol pyruvate carboxykinase,

10.6 the poxB gene which codes for pyruvate oxidase,

10.7 the aceA gene which codes for isocitrate lyase,

10.8 the dgsA gene which codes for the DgsA regulator of the phosphotransferase system,

10.9 the fruR gene which codes for the fructose repressor,

10.10 the rpoS gene which codes for the sigma$^{38}$ factor,

10.11 the aspA gene which codes for aspartate ammonium lyase (aspartase) and

10.12 the aceB gene which codes for malate synthase A

is or are attenuated, in particular eliminated or reduced in expression, are fermented.